

### **Appendix S3** Reconstruction of a dated phylogeny of Dutch angiosperm species

Details of analyses on reconstruction of a dated phylogeny of Dutch angiosperms and justification of methods of dating analyses are provided in (Hermant *et al.*, 2012). In brief, they started by focusing on phylogenetic relationships at the level of all families, which can be represented by sequences of the same gene, *rbcL*, and then proceeded to genera within larger families, to species within older genera and finally to extrapolation of species within all genera. For their dating analyses, in a similar way, they first obtained age estimates for diversifications among all families and genera within the small families in the sample. These reconstructions were based on the same phylogeny and the same gene (*rbcL*) and created a set of reference nodes for calibration of the stem nodes of the large families and old genera, present in the Netherlands. The set of reference nodes was used for age estimations within these taxa. This approach ensures that age estimates for genera and species are comparable across families, since ages of all families are derived from the same basic node age estimates. They also excluded exotic species, and we used the same sample of species (see Methods, ‘Defining and characterizing habitat types’, of the main text).

Ages of stem nodes, estimated on their ‘family tree’, served Hermant *et al.* (2012) as internal calibration points for dating phylogenies within 24 large families (Fig. E2 in Hermant *et al.* (2012)). The topology of the ‘family tree’ served the authors to select the proper outgroups for each of the large families. In these analyses, they used a majority-rule consensus tree of each of family, obtained in Bayesian analyses, and PL method of dating (as described above for the ‘family tree’). The 24 individual dated trees of large families could be grafted into the dated ‘family tree’ using Tree Edit (<http://tree.bio.ed.ac.uk/software/treededit>). This procedure resulted in a dated tree of 555 genera out of the total 557 genera from the sample of Dutch angiosperms.

Preliminary visual inspection of the dated tree of all genera (including representatives of two genera without sequence information, see Fig. E3 in Hermant *et al.* (2012)) indicated, that the stem ages of some of genera were relatively old (up to 100 Ma and more). Treating the clades within these old genera as unresolved could lead to a considerable overestimation of the stem node ages of species from these genera (see below) and to a bias in the patterns of lineage diversification in old epochs of angiosperm evolution. We therefore created additional datasets (similarly to those for large families) to reconstruct phylogenetic relationships and to obtain estimates of ages of diversifications in trees within old genera (specified as those with the stem node age above 35 Ma, Fig. E3 in Hermant *et al.* (2012)). These genera were analyzed separately from all other genera to avoid introducing large proportion of missing data into the total data set. Phylogenetic and dating reconstructions within these old genera followed the same steps as in the analyses of large families. The 34 individual dated trees of 38 old genera (in four cases two old genera were included into the same data set) could be grafted into the dated ‘family tree’, similarly to the trees of genera within large families. In seven old genera, DNA sequences could not be found in Gene Bank for almost all or at least for some species from our sample. Trees of these genera were therefore left partly unresolved. The additional analyses within old genera provided a better resolution within the whole tree and restricted unresolved intrageneric age variation to less than 35 Ma for almost all genera. Finally, all species from remaining (younger) genera were grafted into the tree as unresolved polytomies, in which ages of the crown nodes were defined as half of ages of the correspondent stem nodes of genera.

A dated tree in Newick format with all genera and species represented is available from the TreeBase ID: S13572. The tree is highly congruent with, but often more resolved than that of Durka & Michalski (2012) for the larger region of Europe. The tree is also congruent with that of Zanne *et al.* (2014). Zanne *et al.*’s tree covers some 10-15% of the global Angiosperm flora, which renders it inevitably less complete and representative of the Dutch genera than the complete tree we used.

We note that estimation of age of the crown node of Angiospermae from dating molecular phylogenies is still an issue of considerable uncertainty (Bell *et al.*, 2010; Smith *et al.*, 2010; Magallon *et al.*, 2013). However, the congruence among several dated molecular reconstructions of the earliest evolution in Eudicotyledoneae and paleobotanic records (Doyle & Hotton, 1991) suggest that this age estimate provides a robust constraint for calibrating phylogenies in this large taxon (see also Magallon *et al.*, 2013). We therefore used this estimate as a fixed age constraint for the crown node of Eudicotyledoneae in our dating analyses of Dutch angiosperms. Hermant *et al.* (2012, Appendix E) provide details on other node calibrations.

Our analyses are based on a regional sample as global samples are not available yet for the level of resolution at which we dated phylogenetic relationships, i.e. within most of genera in Dutch angiosperms. It is obvious that our tree is a small subsample of the tree of Angiosperms, especially at the level of species (1,283 out of approximately 352,000; The Plant List, accessed in July 2015) and genera (557 out of 14,559; The Plant List, accessed in July 2015). Representation increases with taxonomic level: 107 out of 405 families (The Plant List, accessed in July 2015); 47 out of 66 orders (Stevens, 2001 onwards), 12 out of 12 subclasses (Thorne & Reveal, 2007). Ages of particular lineages inferred from such a regional sample may not ideally represent their global ages and diversifications. Hence, strictly spoken, our ‘lineage diversities dating back to a given epoch’ in the main text are ‘lineage diversities dating back to a given epoch within the regional flora’. However, the regional sampling only seems to have little impact on the age estimates, among others because our fossil time-calibration points are globally applicable. In fact, Hermant *et al.* (2012) have demonstrated (their Table E3) that age estimates of families in our tree of Dutch angiosperms are generally close to those from a global sample.

We note also that 51% of species in the tree belong to genera with partly unresolved phylogenetic relationships, but the unresolved polytomies were found almost exclusively in two youngest geological epochs from the Neogene (98% of all polytomies).

In an attempt to evaluate a possible impact of unresolved phylogenetic relationships in our tree on our estimates, we obtained 100 trees with randomly resolved polytomies. We used Mesquite (v. 3.03, Maddison & Maddison, 2015) and option 'Randomly Resolve Polytomies' in this software. Randomly resolved branches were joined together by the software such that the new ancestral branch was half the length of the shorter of the two sister branches, and each sister branch was shortened accordingly to maintain height from the root (Proportion of Height from Polytomy=0.5). We generated 100 trees with randomly resolved polytomies and used these trees in our analyses (see Methods). Nevertheless, further efforts to truly (rather than randomly) resolve all remaining polytomies in the tree can potentially allow a more detailed insight into the representation of recent evolutionary heritage in habitat types, notably that from the most recent five million years.

Finally, we note that the aim of our reconstructions was to provide phylogenetic information for tests on differential representation of lineages from different past epochs in distinct regional habitat types, not to measure global diversification rates of lineages in each particular epoch. The latter task would obviously be out of the scope of any regional subsample of the total tree of Angiosperms.